



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:28 AM UTC

PDB ID : 3NIF / pdb_00003nif
Title : The Closed Headpiece of Integrin Iib 3 and its Complex with an Iib 3 -Specific Antagonist That Does Not Induce Opening
Authors : Zhu, J.H.; Zhu, J.Q.; Springer, T.A.
Deposited on : 2010-06-15
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

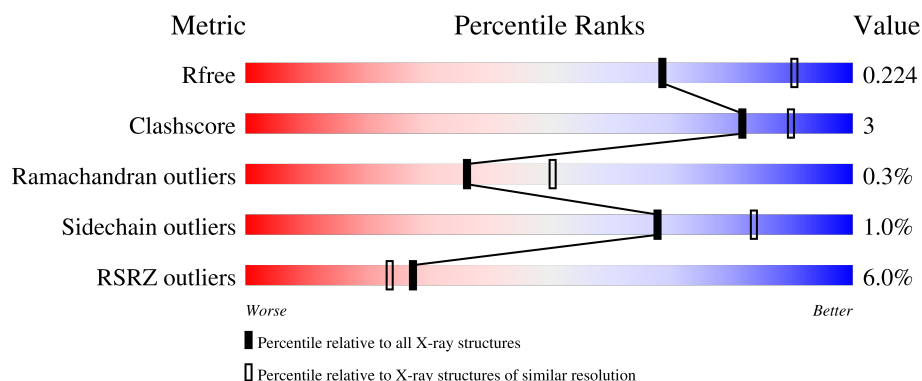
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



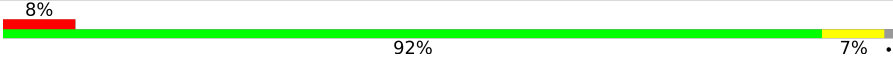
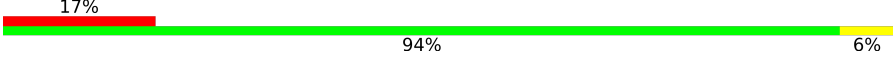
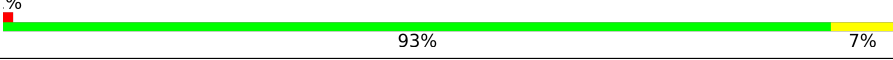
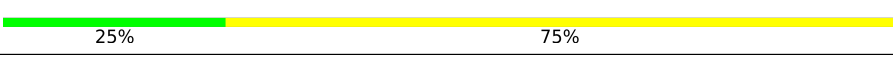
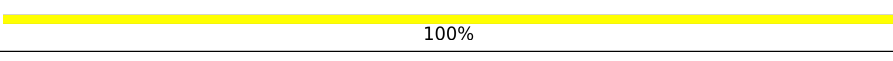
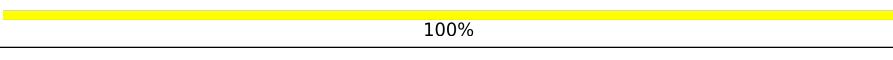
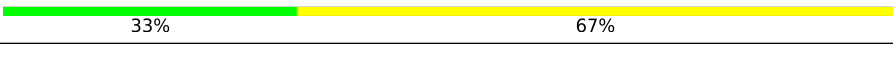
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	457	95%
1	C	457	93% 6%
2	B	471	4% 91% 8%
2	D	471	3% 91% 8%
3	E	221	29% 86% 11%

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Mol	Chain	Length	Quality of chain
3	H	221	
4	F	214	
4	L	214	
5	G	4	
6	I	2	
6	K	2	
7	J	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	NAG	D	3099	X	-	-	-
5	MAN	G	3	X	-	-	-
6	NAG	K	1	X	-	-	-
7	MAN	J	3	X	-	-	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 21915 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Integrin alphaIIB beta3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	3	0
			3501	2225	605	663	8			
1	C	453	Total	C	N	O	S	0	1	0
			3481	2212	600	661	8			

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	466	Total	C	N	O	S	0	0	0
			3590	2236	613	708	33			
2	D	467	Total	C	N	O	S	0	2	0
			3615	2256	616	710	33			

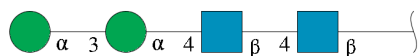
- Molecule 3 is a protein called Monoclonal antibody 10E5 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	216	Total	C	N	O	S	0	0	0
			1638	1039	263	330	6			
3	H	219	Total	C	N	O	S	0	1	0
			1665	1055	270	334	6			

- Molecule 4 is a protein called Monoclonal antibody 10E5 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			
4	L	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



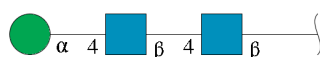
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
6	K	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

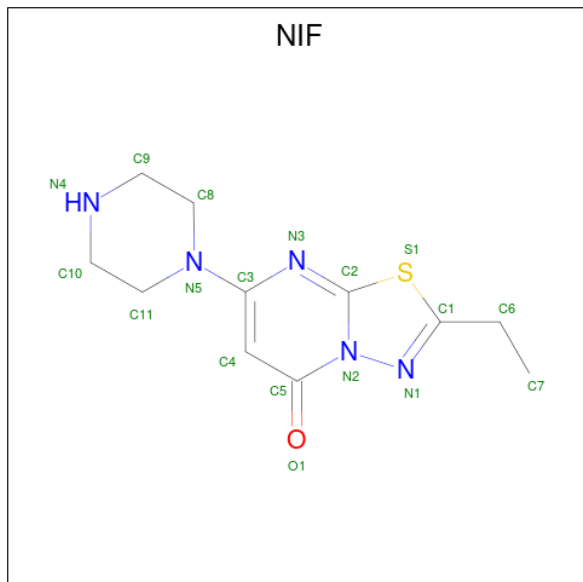


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

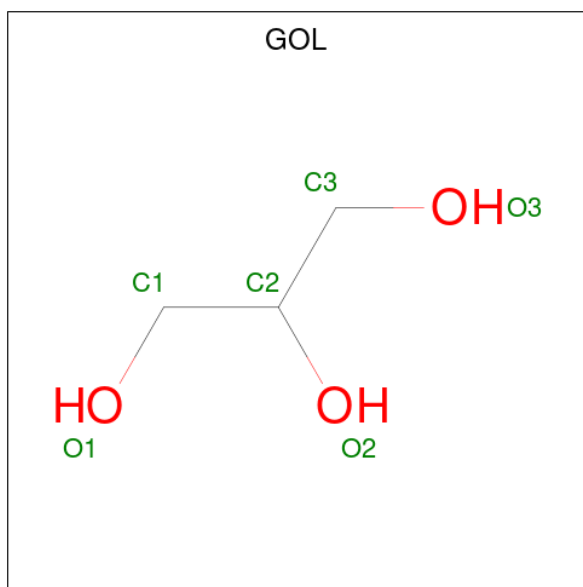
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	4	Total	Ca	0	0
			4	4		
8	B	2	Total	Ca	0	0
			2	2		
8	C	4	Total	Ca	0	0
			4	4		
8	D	2	Total	Ca	0	0
			2	2		

- Molecule 9 is 2-ethyl-7-piperazin-1-yl-5H-[1,3,4]thiadiazolo[3,2-a]pyrimidin-5-one (CCD ID: NIF) (formula: $C_{11}H_{15}N_5OS$).



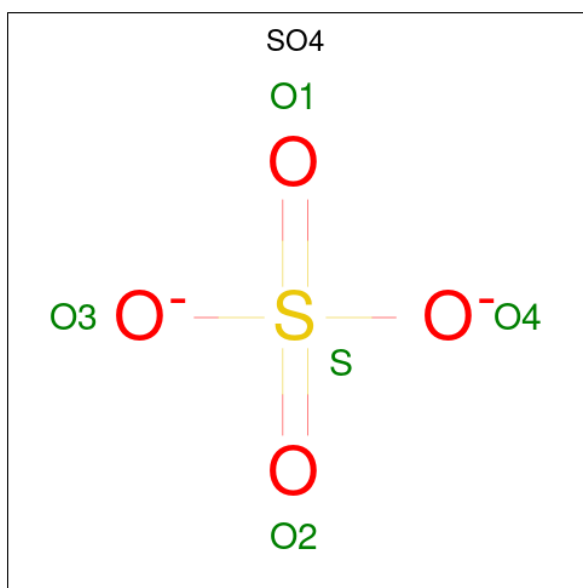
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	S	0	0
			18	11	5	1	1		
9	C	1	Total	C	N	O	S	0	0
			18	11	5	1	1		

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C O 6 3 3	0	0
10	A	1	Total C O 6 3 3	0	0
10	A	1	Total C O 6 3 3	0	0
10	A	1	Total C O 6 3 3	0	0
10	A	1	Total C O 6 3 3	0	0
10	A	1	Total C O 6 3 3	0	0
10	B	1	Total C O 6 3 3	0	0
10	D	1	Total C O 6 3 3	0	0

- Molecule 11 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total O S 5 4 1	0	0
11	A	1	Total O S 5 4 1	0	0
11	A	1	Total O S 5 4 1	0	0
11	A	1	Total O S 5 4 1	0	0

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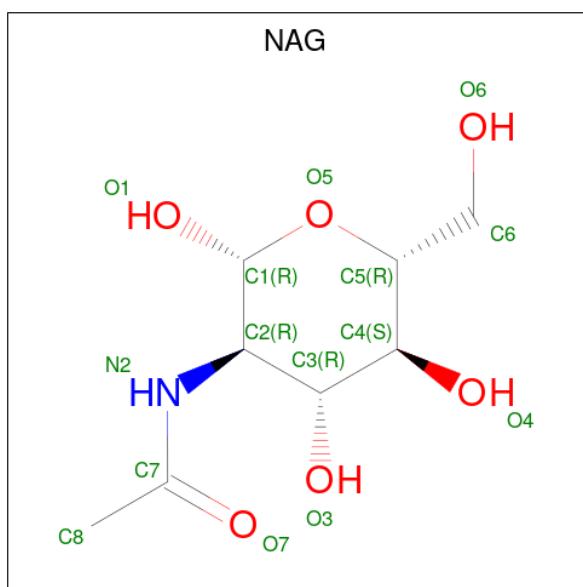
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	O	S	0	0
			5	4	1		
11	B	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	C	1	Total	O	S	0	0
			5	4	1		
11	D	1	Total	O	S	0	0
			5	4	1		
11	D	1	Total	O	S	0	0
			5	4	1		
11	D	1	Total	O	S	0	0
			5	4	1		
11	H	1	Total	O	S	0	0
			5	4	1		
11	L	1	Total	O	S	0	0
			5	4	1		
11	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	B	1	Total	Mg	0	0
			1	1		
12	D	1	Total	Mg	0	0
			1	1		

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	B	1	Total	C	N	O	0	0
			14	8	1	5		
13	D	1	Total	C	N	O	0	0
			14	8	1	5		

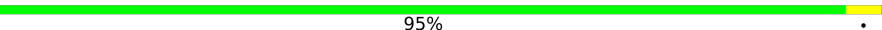
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	277	Total	O	0	0
			277	277		
14	B	175	Total	O	0	0
			175	175		
14	C	140	Total	O	0	0
			140	140		
14	D	110	Total	O	0	0
			110	110		
14	E	9	Total	O	0	0
			9	9		
14	F	6	Total	O	0	0
			6	6		
14	H	29	Total	O	0	0
			29	29		
14	L	44	Total	O	0	0
			44	44		

3 Residue-property plots

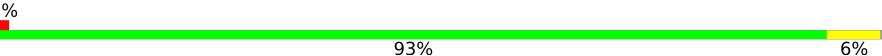
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

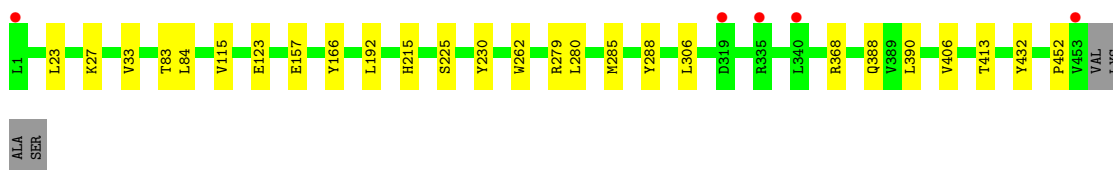
- Molecule 1: Integrin alphaIIB beta3

Chain A:  95%



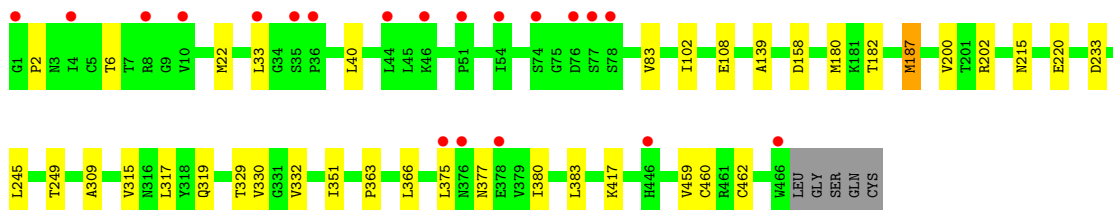
- Molecule 1: Integrin alphaIIB beta3

Chain C:  93% 6%

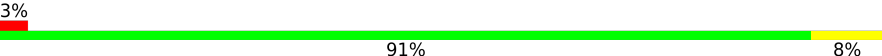


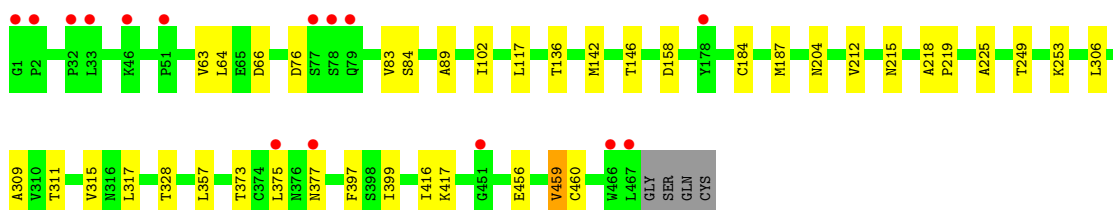
- Molecule 2: Integrin beta-3

Chain B:  91% 8% 4%

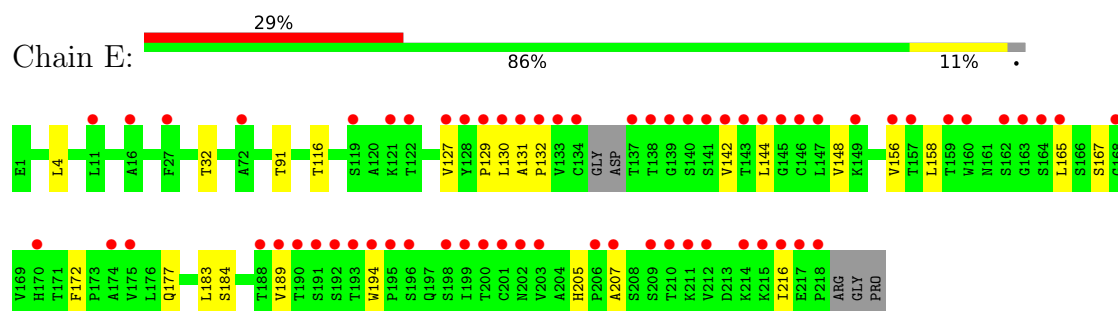


- Molecule 2: Integrin beta-3

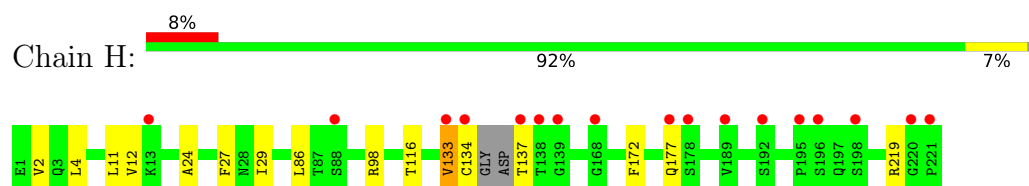
Chain D:  91% 8% 3%



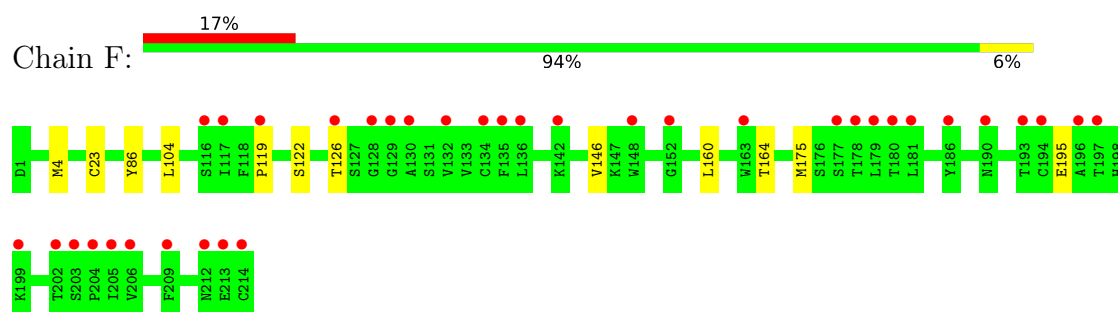
- Molecule 3: Monoclonal antibody 10E5 heavy chain



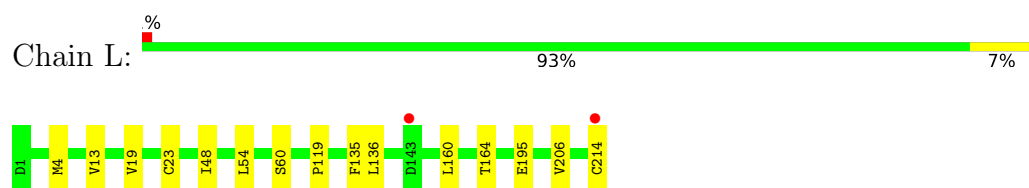
- Molecule 3: Monoclonal antibody 10E5 heavy chain



- Molecule 4: Monoclonal antibody 10E5 light chain



- Molecule 4: Monoclonal antibody 10E5 light chain



- Molecule 5: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%

MAG1
MAG2

- Molecule 7: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  33% 67%

MAG1
MAG2
MAN3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	259.53Å 144.28Å 104.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.21 – 2.40 48.21 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.1 (48.21-2.40) 95.1 (48.21-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0093	Depositor
R, R_{free}	0.176 , 0.216 (Not available) , 0.224	Depositor DCC
R_{free} test set	860 reflections (0.59%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	21915	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, NAG, NIF, GOL, SO4, MAN, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/3607	0.71	0/4915
1	C	0.51	0/3581	0.69	0/4880
2	B	0.52	0/3657	0.73	1/4959 (0.0%)
2	D	0.49	0/3690	0.71	0/5005
3	E	0.46	0/1680	0.64	0/2301
3	H	0.42	0/1711	0.62	0/2343
4	F	0.45	0/1673	0.61	0/2269
4	L	0.43	0/1673	0.62	0/2269
All	All	0.50	0/21272	0.68	1/28941 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	180	MET	N-CA-C	-5.45	101.42	109.86

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3501	0	3343	12	0
1	C	3481	0	3316	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3590	0	3511	17	0
2	D	3615	0	3540	20	0
3	E	1638	0	1594	20	0
3	H	1665	0	1623	10	0
4	F	1637	0	1553	8	0
4	L	1637	0	1553	10	0
5	G	50	0	43	0	0
6	I	28	0	25	0	0
6	K	28	0	25	0	0
7	J	39	0	34	0	0
8	A	4	0	0	0	0
8	B	2	0	0	0	0
8	C	4	0	0	0	0
8	D	2	0	0	0	0
9	A	18	0	15	0	0
9	C	18	0	15	3	0
10	A	36	0	48	1	0
10	B	6	0	8	0	0
10	D	6	0	8	0	0
11	A	25	0	0	0	0
11	B	5	0	0	0	0
11	C	30	0	0	0	0
11	D	15	0	0	0	0
11	H	5	0	0	0	0
11	L	10	0	0	0	0
12	B	1	0	0	0	0
12	D	1	0	0	0	0
13	B	14	0	13	0	0
13	D	14	0	13	0	0
14	A	277	0	0	0	0
14	B	175	0	0	1	0
14	C	140	0	0	1	0
14	D	110	0	0	0	0
14	E	9	0	0	0	0
14	F	6	0	0	0	0
14	H	29	0	0	0	0
14	L	44	0	0	0	0
All	All	21915	0	20280	105	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 105 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:4:MET:HE3	4:F:23:CYS:SG	2.24	0.77
4:L:4:MET:HE3	4:L:23:CYS:SG	2.26	0.76
3:H:133:VAL:HG21	4:L:119:PRO:HG2	1.71	0.72
3:E:144:LEU:HD22	3:E:216:ILE:HG21	1.74	0.70
2:B:22:MET:HE2	2:B:40:LEU:HD21	1.72	0.69

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	455/457 (100%)	441 (97%)	13 (3%)	1 (0%)	43	58
1	C	452/457 (99%)	437 (97%)	14 (3%)	1 (0%)	43	58
2	B	464/471 (98%)	442 (95%)	20 (4%)	2 (0%)	30	43
2	D	467/471 (99%)	448 (96%)	16 (3%)	3 (1%)	21	32
3	E	212/221 (96%)	191 (90%)	20 (9%)	1 (0%)	24	37
3	H	216/221 (98%)	203 (94%)	12 (6%)	1 (0%)	24	37
4	F	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
4	L	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
All	All	2690/2726 (99%)	2570 (96%)	111 (4%)	9 (0%)	36	50

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
1	C	123	GLU
2	D	375	LEU
2	D	76	ASP
3	E	167	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	365/364 (100%)	360 (99%)	5 (1%)	59	79
1	C	362/364 (100%)	358 (99%)	4 (1%)	65	82
2	B	412/416 (99%)	404 (98%)	8 (2%)	50	71
2	D	415/416 (100%)	410 (99%)	5 (1%)	63	81
3	E	187/190 (98%)	187 (100%)	0	100	100
3	H	190/190 (100%)	190 (100%)	0	100	100
4	F	188/188 (100%)	188 (100%)	0	100	100
4	L	188/188 (100%)	187 (100%)	1 (0%)	81	91
All	All	2307/2316 (100%)	2284 (99%)	23 (1%)	68	84

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	157	GLU
2	D	84	SER
1	C	288	TYR
2	D	215	ASN
2	B	182	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	L	37	GLN
4	L	190	ASN
4	L	93	GLN
2	D	204	ASN
3	H	39	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

11 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	1	5,2	14,14,15	0.63	0	17,19,21	1.14	1 (5%)
5	NAG	G	2	5	14,14,15	0.62	0	17,19,21	0.91	1 (5%)
5	MAN	G	3	5	11,11,12	0.61	0	15,15,17	0.85	1 (6%)
5	MAN	G	4	5	11,11,12	0.53	0	15,15,17	0.66	0
6	NAG	I	1	6,2	14,14,15	0.62	0	17,19,21	1.25	2 (11%)
6	NAG	I	2	6	14,14,15	0.51	0	17,19,21	1.27	1 (5%)
7	NAG	J	1	7,2	14,14,15	0.48	0	17,19,21	1.00	2 (11%)
7	NAG	J	2	7	14,14,15	0.61	0	17,19,21	0.92	0
7	MAN	J	3	7	11,11,12	0.52	0	15,15,17	1.73	2 (13%)
6	NAG	K	1	6,2	14,14,15	0.44	0	17,19,21	0.91	1 (5%)
6	NAG	K	2	6	14,14,15	0.45	0	17,19,21	0.98	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	G	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	MAN	G	3	5	1/1/4/5	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	J	1	7,2	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	MAN	J	3	7	1/1/4/5	1/2/19/22	1/1/1/1
6	NAG	K	1	6,2	1/1/5/7	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	3	MAN	C1-O5-C5	5.29	119.27	112.19
6	I	1	NAG	C3-C4-C5	3.12	115.90	110.23
6	I	2	NAG	O5-C1-C2	-3.10	106.49	111.29
7	J	3	MAN	C1-C2-C3	2.81	113.74	109.64
6	K	1	NAG	C1-O5-C5	2.74	115.86	112.19

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	G	3	MAN	C1
6	K	1	NAG	C1
7	J	3	MAN	C1

5 of 10 torsion outliers are listed below:

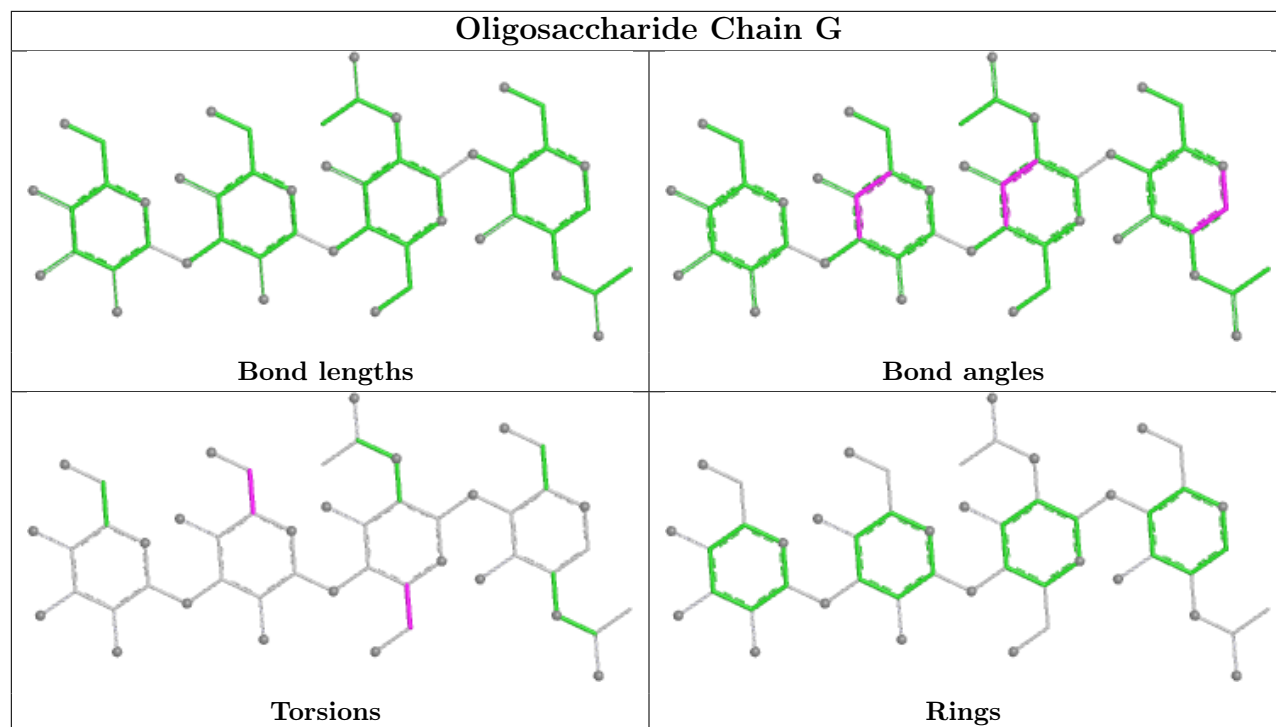
Mol	Chain	Res	Type	Atoms
5	G	3	MAN	C4-C5-C6-O6
5	G	3	MAN	O5-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	K	2	NAG	C8-C7-N2-C2

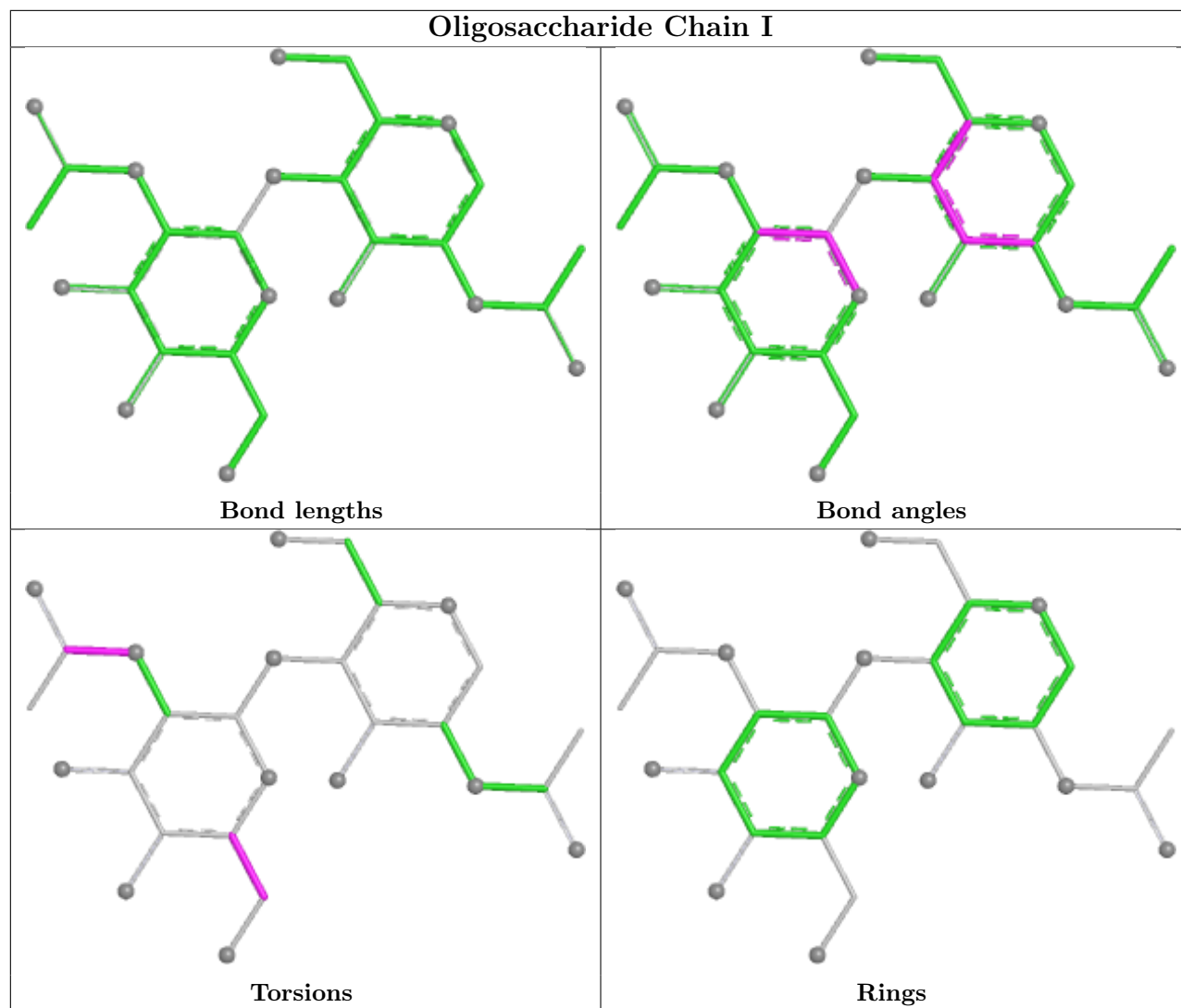
All (1) ring outliers are listed below:

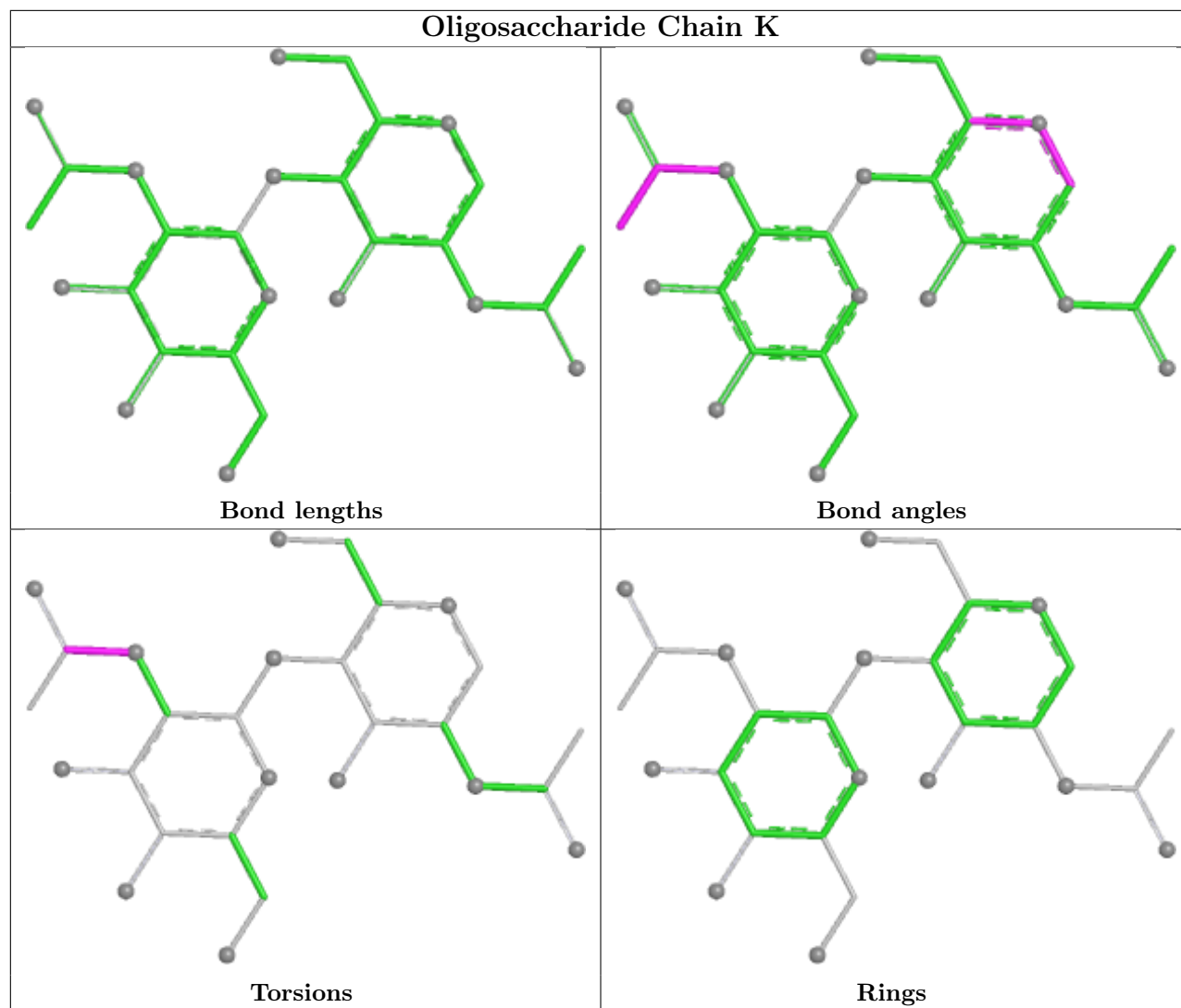
Mol	Chain	Res	Type	Atoms
7	J	3	MAN	C1-C2-C3-C4-C5-O5

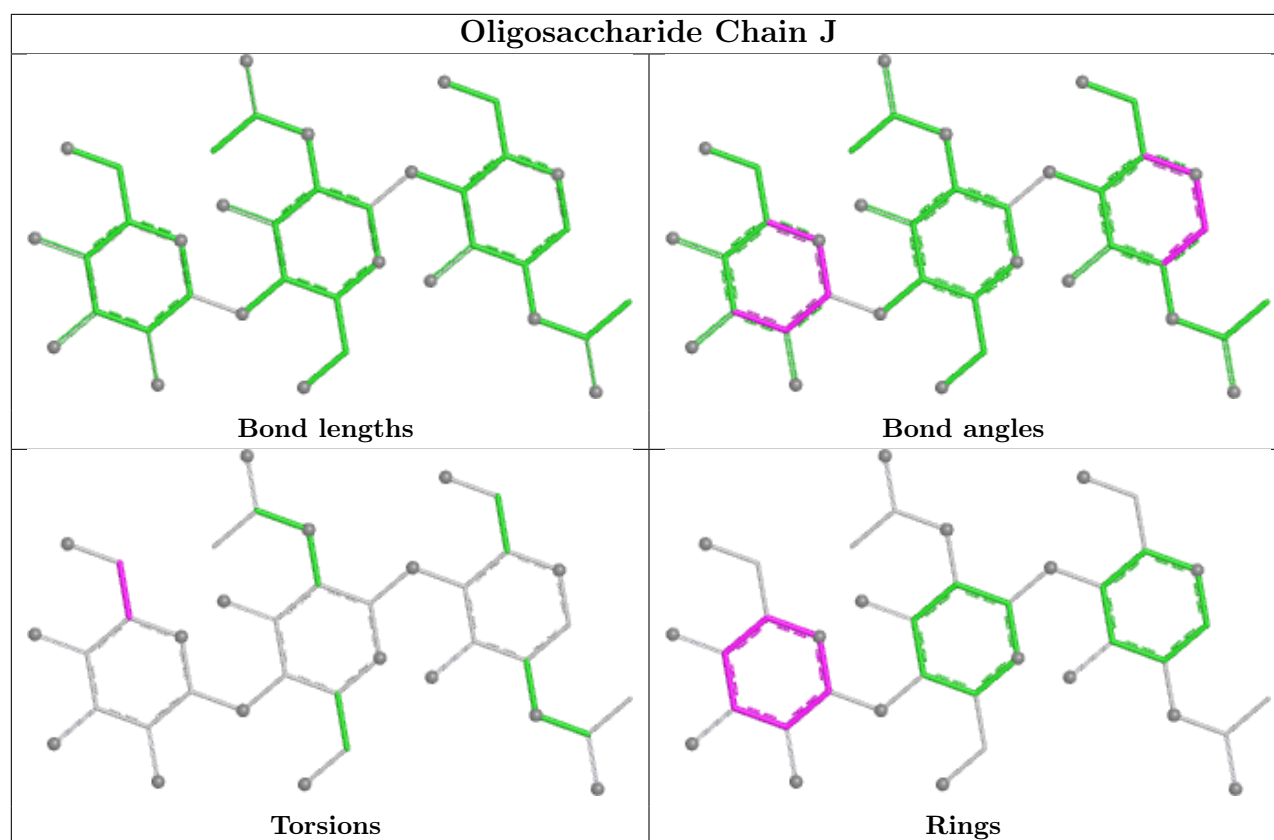
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 14 are monoatomic - leaving 30 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	SO4	L	215	-	4,4,4	0.23	0	6,6,6	0.19	0
9	NIF	C	455	-	20,20,20	3.24	7 (35%)	25,28,28	3.13	12 (48%)
13	NAG	D	3099	2	14,14,15	0.45	0	17,19,21	0.65	0
9	NIF	A	455	-	20,20,20	3.18	8 (40%)	25,28,28	3.00	10 (40%)
13	NAG	B	3099	2	14,14,15	0.51	0	17,19,21	0.96	0
11	SO4	C	456	-	4,4,4	0.25	0	6,6,6	0.31	0
11	SO4	C	458	-	4,4,4	0.26	0	6,6,6	0.16	0
11	SO4	H	222	-	4,4,4	0.24	0	6,6,6	0.13	0
11	SO4	A	463	-	4,4,4	0.30	0	6,6,6	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	GOL	B	472	-	5,5,5	0.39	0	5,5,5	0.18	0
11	SO4	A	462	-	4,4,4	0.26	0	6,6,6	0.06	0
11	SO4	C	459	-	4,4,4	0.24	0	6,6,6	0.07	0
11	SO4	D	475	-	4,4,4	0.26	0	6,6,6	0.16	0
11	SO4	D	474	-	4,4,4	0.22	0	6,6,6	0.13	0
11	SO4	A	466	-	4,4,4	0.24	0	6,6,6	0.10	0
10	GOL	A	458	-	5,5,5	0.39	0	5,5,5	0.28	0
11	SO4	D	473	-	4,4,4	0.22	0	6,6,6	0.22	0
11	SO4	A	465	-	4,4,4	0.26	0	6,6,6	0.13	0
10	GOL	A	456	-	5,5,5	0.32	0	5,5,5	0.25	0
10	GOL	A	459	-	5,5,5	0.40	0	5,5,5	0.74	0
11	SO4	A	464	-	4,4,4	0.30	0	6,6,6	0.15	0
10	GOL	D	472	-	5,5,5	0.37	0	5,5,5	0.22	0
11	SO4	C	460	-	4,4,4	0.28	0	6,6,6	0.14	0
11	SO4	C	461	-	4,4,4	0.23	0	6,6,6	0.11	0
11	SO4	C	457	-	4,4,4	0.22	0	6,6,6	0.32	0
11	SO4	B	473	-	4,4,4	0.27	0	6,6,6	0.15	0
11	SO4	L	216	-	4,4,4	0.25	0	6,6,6	0.10	0
10	GOL	A	461	-	5,5,5	0.38	0	5,5,5	0.77	0
10	GOL	A	460	-	5,5,5	0.28	0	5,5,5	0.66	0
10	GOL	A	457	-	5,5,5	0.33	0	5,5,5	0.31	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	GOL	A	458	-	-	0/4/4/4	-
10	GOL	A	456	-	-	2/4/4/4	-
9	NIF	C	455	-	-	2/6/14/14	0/3/3/3
10	GOL	A	459	-	-	2/4/4/4	-
13	NAG	D	3099	2	1/1/5/7	0/6/23/26	0/1/1/1
10	GOL	B	472	-	-	2/4/4/4	-
9	NIF	A	455	-	-	1/6/14/14	0/3/3/3
10	GOL	D	472	-	-	2/4/4/4	-
13	NAG	B	3099	2	-	0/6/23/26	0/1/1/1
10	GOL	A	461	-	-	2/4/4/4	-
10	GOL	A	460	-	-	0/4/4/4	-
10	GOL	A	457	-	-	0/4/4/4	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	455	NIF	C3-N3	7.83	1.51	1.36
9	C	455	NIF	C1-S1	7.79	1.86	1.74
9	A	455	NIF	C3-N3	7.74	1.51	1.36
9	A	455	NIF	C1-S1	7.05	1.85	1.74
9	A	455	NIF	C1-N1	6.37	1.34	1.29

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	455	NIF	S1-C1-N1	-7.08	110.75	116.60
9	C	455	NIF	C4-C3-N3	-7.04	118.12	122.86
9	A	455	NIF	S1-C1-N1	-6.32	111.38	116.60
9	A	455	NIF	C4-C3-N3	-5.90	118.89	122.86
9	C	455	NIF	N2-C2-N3	-5.78	120.72	125.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	D	3099	NAG	C1

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	459	GOL	O1-C1-C2-C3
10	B	472	GOL	C1-C2-C3-O3
10	A	459	GOL	O1-C1-C2-O2
10	A	456	GOL	O1-C1-C2-C3
10	A	461	GOL	C1-C2-C3-O3

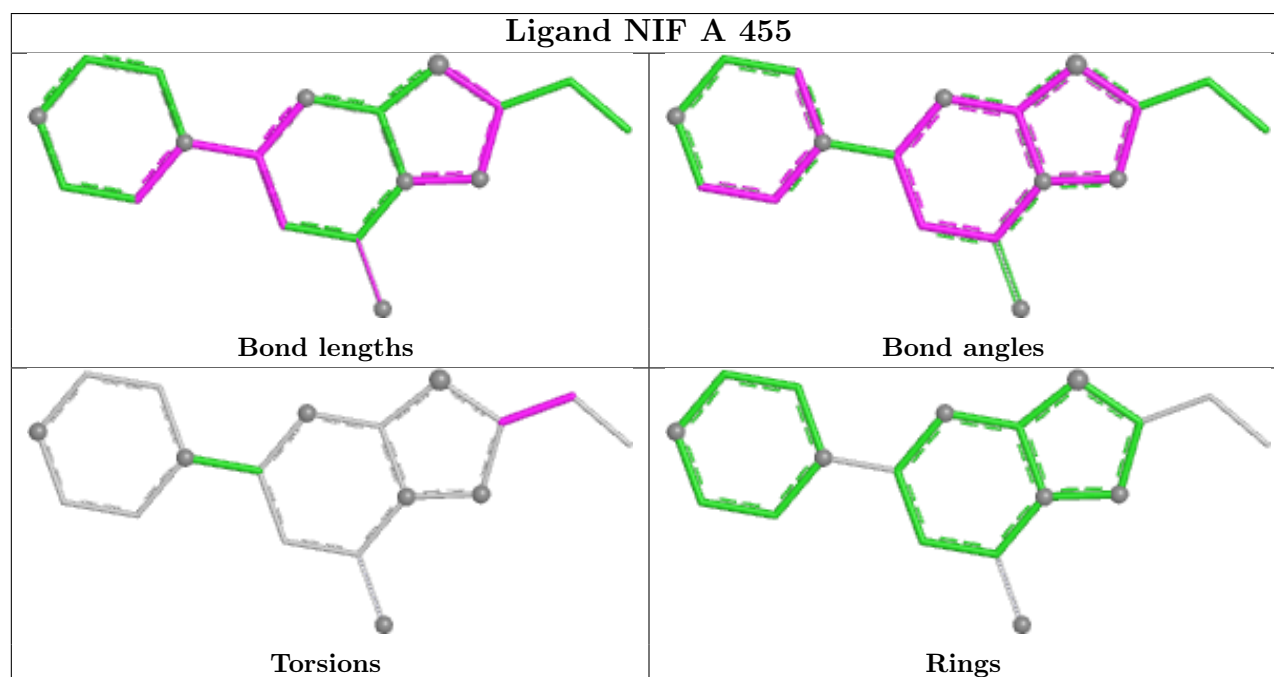
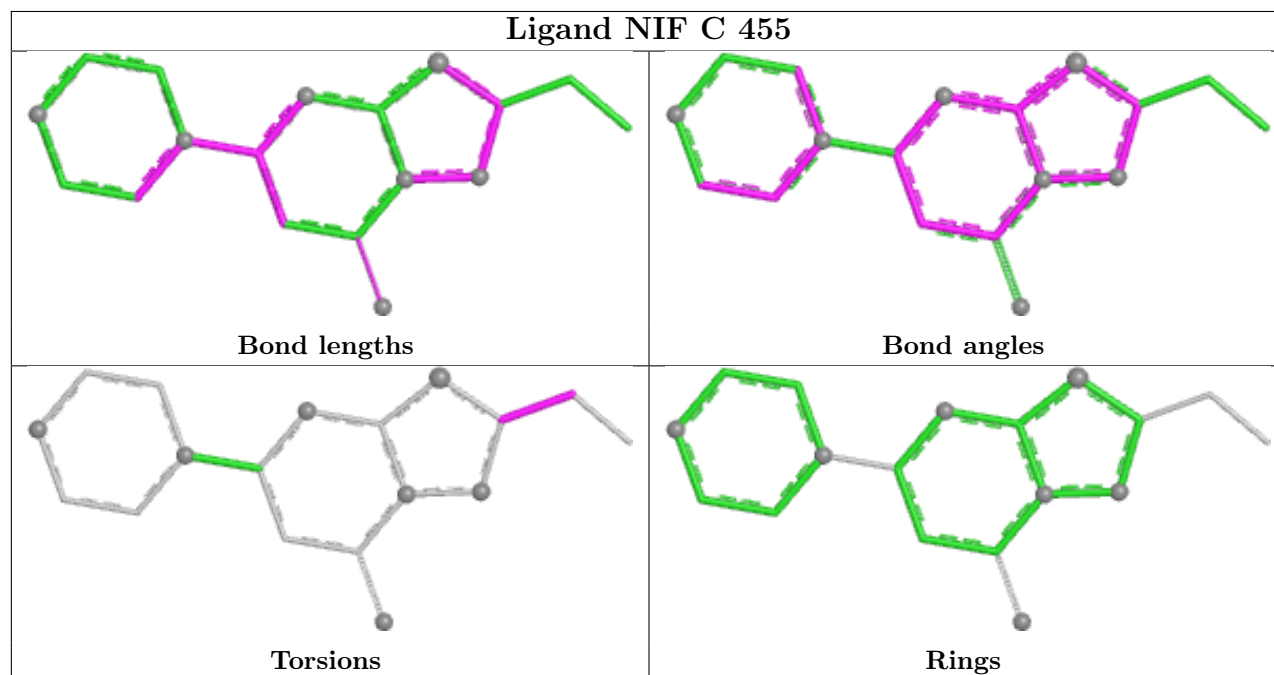
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	C	455	NIF	3	0
10	A	457	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	454/457 (99%)	-0.74	2 (0%) 88 86	12, 20, 47, 84	3 (0%)
1	C	453/457 (99%)	-0.41	5 (1%) 78 74	19, 35, 64, 102	1 (0%)
2	B	466/471 (98%)	-0.00	20 (4%) 40 36	12, 45, 134, 189	0
2	D	467/471 (99%)	0.03	15 (3%) 50 46	17, 48, 109, 151	2 (0%)
3	E	216/221 (97%)	1.51	65 (30%) 1 1	45, 120, 192, 220	0
3	H	219/221 (99%)	0.53	17 (7%) 19 15	27, 73, 140, 166	2 (0%)
4	F	214/214 (100%)	0.98	36 (16%) 4 3	44, 102, 170, 248	1 (0%)
4	L	214/214 (100%)	0.03	2 (0%) 81 78	30, 60, 100, 147	1 (0%)
All	All	2703/2726 (99%)	0.06	162 (5%) 27 24	12, 48, 147, 248	10 (0%)

The worst 5 of 162 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	221	PRO	5.7
3	E	212	VAL	5.6
3	E	165	LEU	5.4
3	E	199	ILE	5.2
2	B	33	LEU	5.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

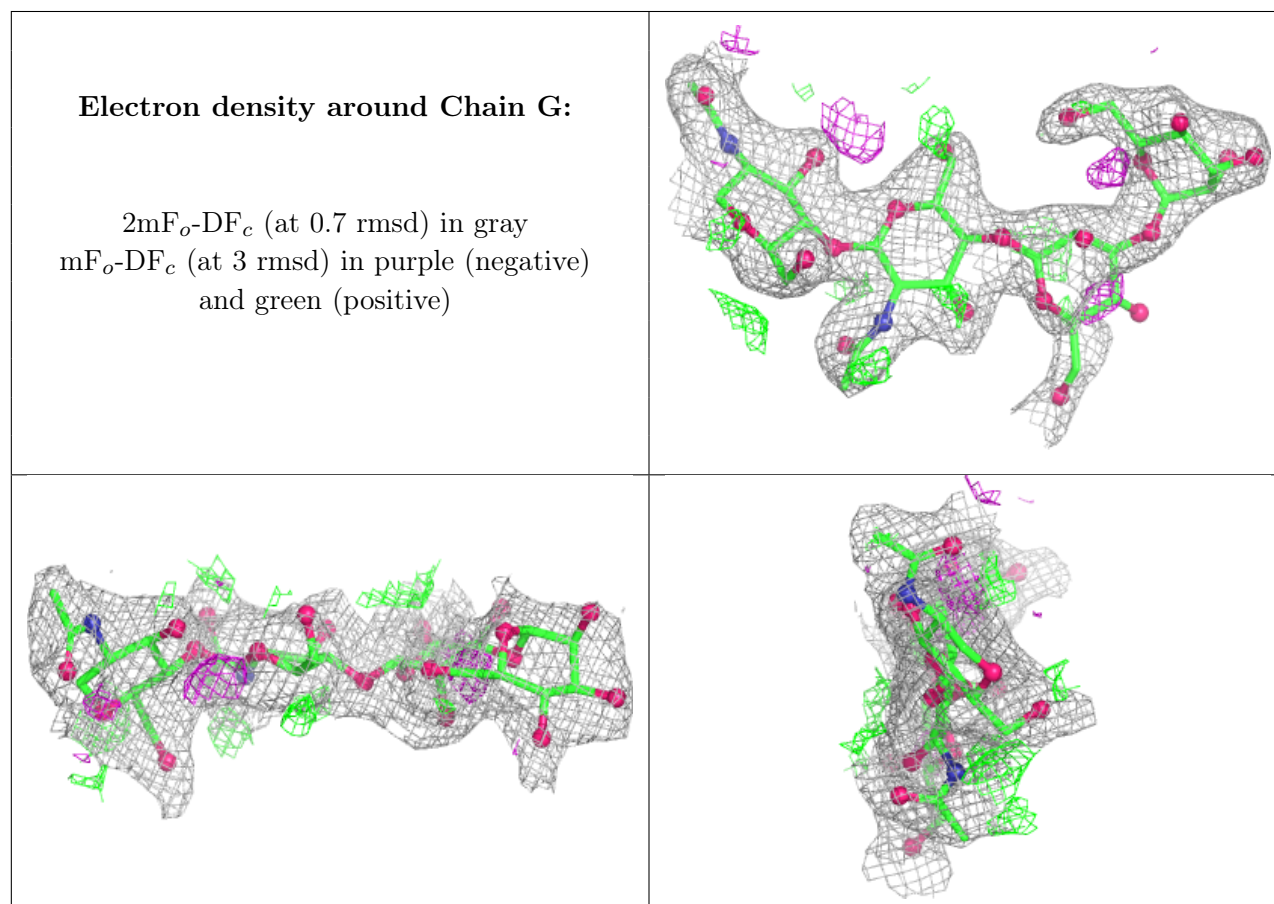
6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

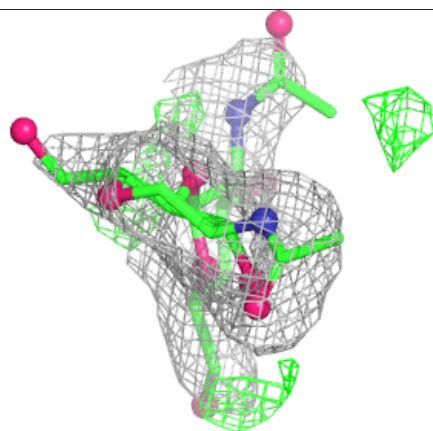
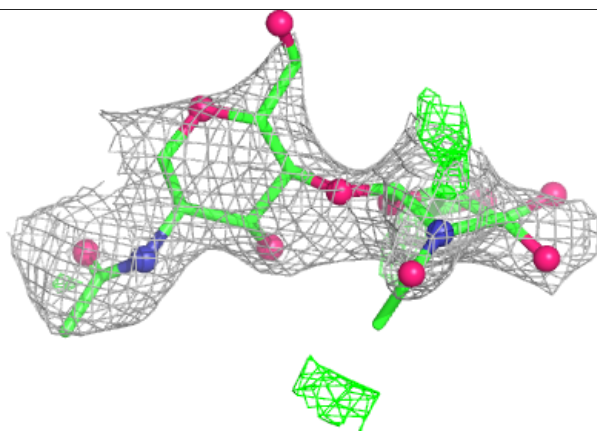
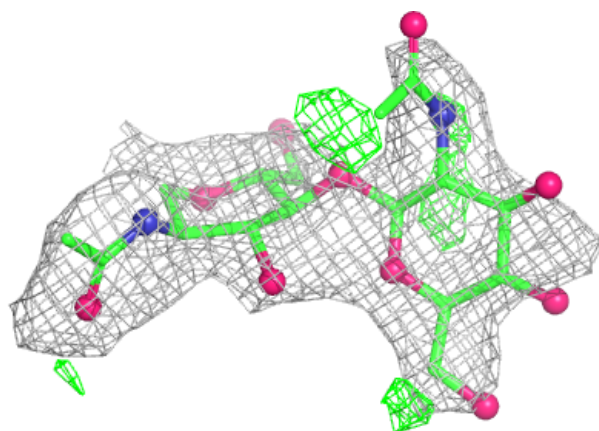
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	G	1	14/15	-	-	21,34,49,49	0
5	NAG	G	2	14/15	-	-	44,58,70,80	0
5	MAN	G	3	11/12	-	-	76,98,105,108	0
5	MAN	G	4	11/12	-	-	80,95,99,100	0
7	NAG	J	2	14/15	0.56	0.20	52,77,92,102	0
7	NAG	J	1	14/15	0.84	0.14	36,52,61,64	0
6	NAG	K	2	14/15	0.85	0.14	112,115,120,123	0
6	NAG	I	2	14/15	0.87	0.11	109,116,117,118	0
6	NAG	K	1	14/15	0.92	0.10	63,85,96,106	0
6	NAG	I	1	14/15	0.95	0.08	71,88,99,109	0
7	MAN	J	3	11/12	-	-	98,111,116,118	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

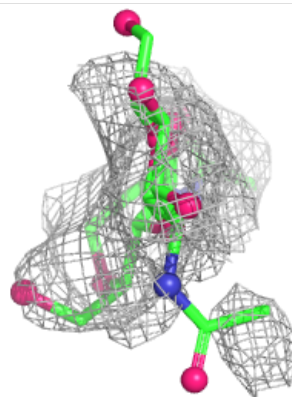
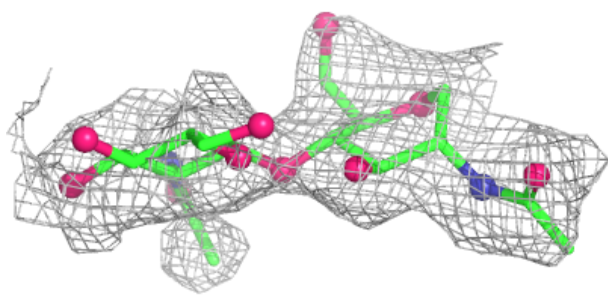
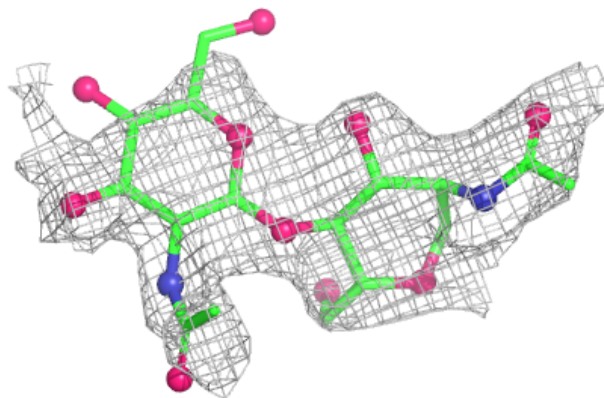


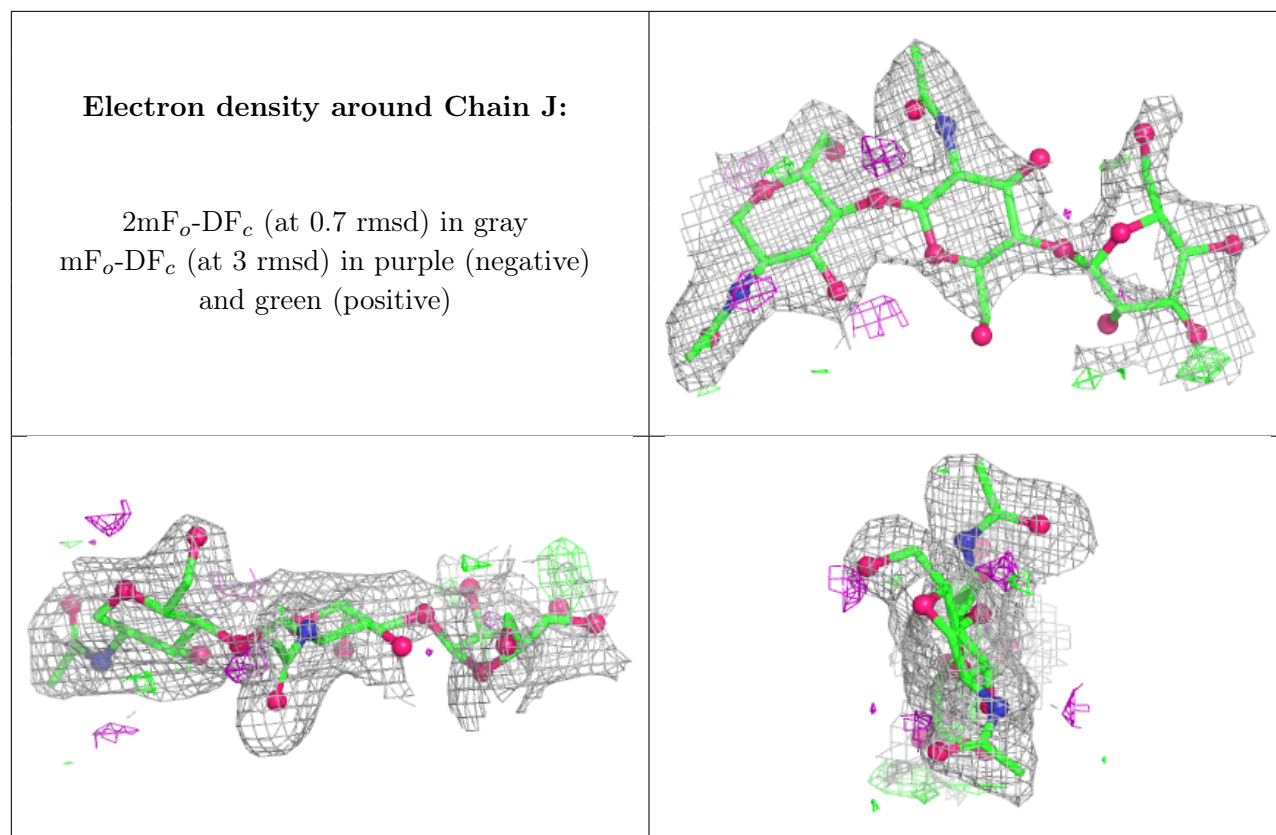
Electron density around Chain I:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Chain K:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	SO4	C	459	5/5	0.65	0.12	109,116,117,119	0
11	SO4	C	461	5/5	0.67	0.14	98,99,101,104	0
11	SO4	A	462	5/5	0.68	0.17	114,115,120,121	0
13	NAG	D	3099	14/15	0.71	0.19	90,101,104,106	0
11	SO4	A	464	5/5	0.72	0.17	82,94,97,97	0
11	SO4	A	463	5/5	0.75	0.17	77,89,96,98	0
11	SO4	C	458	5/5	0.77	0.13	78,89,92,93	0
11	SO4	C	460	5/5	0.78	0.20	93,102,107,114	0
11	SO4	H	222	5/5	0.79	0.14	95,105,107,108	0
11	SO4	L	215	5/5	0.79	0.15	80,90,101,102	0
11	SO4	D	473	5/5	0.79	0.14	101,106,109,109	0
11	SO4	B	473	5/5	0.81	0.18	107,110,116,119	0
10	GOL	A	461	6/6	0.81	0.23	48,52,60,62	0
10	GOL	A	459	6/6	0.81	0.21	67,71,79,81	0

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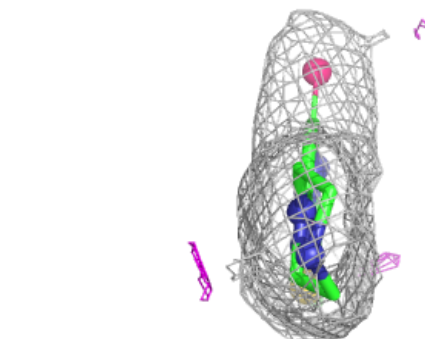
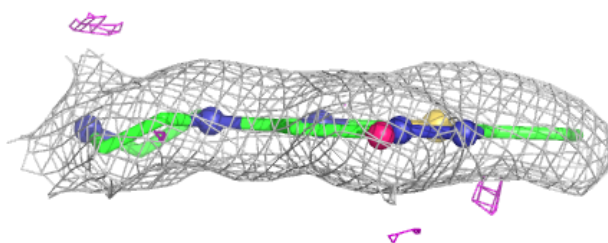
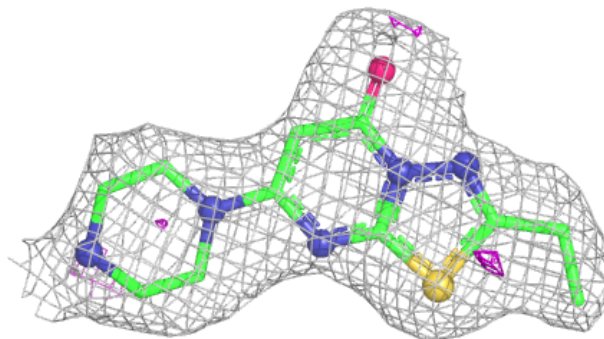
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	SO4	D	475	5/5	0.82	0.21	123,123,125,126	0
13	NAG	B	3099	14/15	0.83	0.13	87,97,105,105	0
11	SO4	L	216	5/5	0.83	0.12	91,93,94,96	0
11	SO4	D	474	5/5	0.84	0.16	115,120,123,123	0
11	SO4	A	465	5/5	0.86	0.15	90,95,96,99	0
11	SO4	A	466	5/5	0.86	0.25	137,139,139,142	0
10	GOL	B	472	6/6	0.86	0.18	75,76,78,79	0
11	SO4	C	457	5/5	0.86	0.21	63,71,86,88	0
10	GOL	D	472	6/6	0.87	0.15	44,55,64,66	0
10	GOL	A	457	6/6	0.87	0.13	33,47,55,57	0
12	MG	D	2001	1/1	0.88	0.20	82,82,82,82	0
10	GOL	A	456	6/6	0.90	0.14	20,42,44,46	0
11	SO4	C	456	5/5	0.91	0.21	56,76,81,84	0
10	GOL	A	460	6/6	0.94	0.12	34,47,61,71	0
10	GOL	A	458	6/6	0.95	0.11	31,47,57,60	0
9	NIF	C	455	18/18	0.95	0.08	31,35,43,44	0
12	MG	B	2001	1/1	0.95	0.08	53,53,53,53	0
8	CA	C	2007	1/1	0.96	0.06	39,39,39,39	0
9	NIF	A	455	18/18	0.97	0.05	19,23,29,30	0
8	CA	C	2004	1/1	0.97	0.04	55,55,55,55	0
8	CA	B	2002	1/1	0.97	0.04	36,36,36,36	0
8	CA	D	2002	1/1	0.97	0.03	36,36,36,36	0
8	CA	A	2004	1/1	0.98	0.03	33,33,33,33	0
8	CA	C	2005	1/1	0.98	0.03	44,44,44,44	0
8	CA	A	2005	1/1	0.99	0.03	24,24,24,24	0
8	CA	A	2006	1/1	0.99	0.04	19,19,19,19	0
8	CA	D	2003	1/1	0.99	0.03	26,26,26,26	0
8	CA	A	2007	1/1	0.99	0.02	18,18,18,18	0
8	CA	C	2006	1/1	0.99	0.05	38,38,38,38	0
8	CA	B	2003	1/1	1.00	0.01	14,14,14,14	0

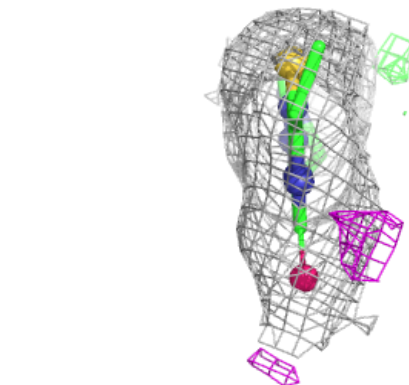
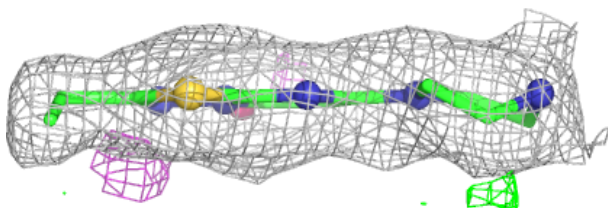
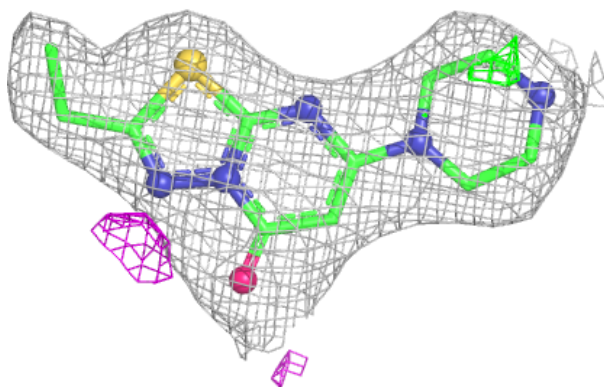
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NIF C 455:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around NIF A 455:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.